101 TCCTGUTTTCAATCTGTTCGTCTGCGAATCGAATTCTTTGTTTTTTTCTCTAATTTTACCGGGAATTGTCGAATTAGGCATTCACCAAGGAGCAAGAG GGATGUAGGTGGCGGGGGGGCTGGGGGCTCTGTACAGGACCTCCGRCTACGCGTGGTGGTGTCCATCAACCTGTTCGTCGCCGCTGCTCTGCGCCTG M R V A A A R L G A L T T S D I A S V Y S I N L F V A L L C A C 401 CATCHTCTCGCCCACCTCCTCGAGGACAATCGCTGGGTCAATGAGTCCATCACCGCGCTCATCATCGGGCTCTGCACCGGCGTGGTGATCTTSCTGATG I A T C H F F B B B B A A A B B I L Y F L L C L C A C A A T F F H 501 ACCARAGGARGAGCTCGCACTTATTCGTCTCAGTGAGGATCTCTTCTTCATCTACCTCCTCCTCCGATCATCTTCAATGCAGGTTTTCAGGTAAAGA TRGKSSHLFVFSEDLFFIILLFFIIFNAGFQVKK 601 AAAAGCARTTCTTCCGGRAFTTCATGACGATCACATTATTTGGAGCCGTCGGGACAATGATATCCTTTTTCACAATATCTATTGCTGCCATTGCAATATT K Q F P R N F H T I T L P G A V C T H I S P F T I S I A A I A I P 701 CAGCAGARTGAACATTGGAACGCTGGATGTAGGAGATTTTCTTGCAATTGGAGCCATCTTTTCTGCGACAGATTCTGTCGCACATTTGCAGCTTCTCTCAAT S R H H I G T L D V G D F L A I G A I F S A T D S V C T L D V L N 801 CAGGATGAGACACCCTTTTTGTACAGTCTGGTATTCGGTGAAGGTGTTGTGAACGATGCTACAACAATTGTGCTTTTCAACGGACTACAGAACTTTGATC Q D E T P F L I S L V F G E G V V N D A T S I V L F N A L Q N F D L V H I D A A V V L K P L G N P F Y L F L S S T P L G V P A G L L S 1001 TGCATACATARTCAAGAAGCTATACATTGGAAGGCATTCTACTGACGGTGAGGTTGCCCTTATGATGGTCATGGCTTACCTTTCATATATGCTGACGTTACC A T I I K K L Y I G R H S T D R E V A L M H L M A Y L S T M L A E $1101 \quad {\tt TIGGTAGATTIGAGGGGGATTCTCACCGTATTCTTGTGGGTATTGTAATGTCACATTACACTTGGGATAACGTCACAGAGAGTTCAAGAGTTACAACAA$ LLDLSGILTVFFCGIVMSHYTWHNVTESSRV H A F A T L S P I A E T F L P L Y V G N D A L D I E K W E P A S D 1301 CAGACCTGGCAAATCCATTGGGATAAGCTCAATTTTGCTAGGATGGTTCTGATTGGAAGAGCTGCTTTTGTATTCCCGCTGTCGTTCTTTGTCCAACCTA RPGRSIGISSILLGLVLIGRAP 1401 ACAAGGAGGCACCGAATGAAAAATAACCTGGGAGCAGCAAGTTGTAATATGGTGGGCTGGGTTGATGAGAGGAGCTGTGTGGATTGCTTTCCTTACA T K K A P N E K I T W R Q Q V V I W N A G L H R G A V S I A L A Y N 1501 ATAGGTTTACAGGTCTGGCCGTACTCAGCTGCACGGCAATGCAATAATGATCACCAGCACCATCACTGTCTTTTTTTAGCACTATGGTATTTTGGGAT K F T R S G H T Q L H G N A I M I T S T I T V V L P S T H V P G H 1601 GATGACANAGCCATTGATCAGGCTGCTGCTGCCGGCCTCAGGGCCATCCTGTCACCACCTCAGGCCTTCATCACCAAAGTCCCTGCATTCTCCTCTGACA M T K P L I R L L P A S G H P V T S E P S S P K S L H S P L L T S N Q G S D L E S T N I V R P S S L R M L L T K P T R T V H Y Y W 1801 GGGCAAGTTCGACGACGCGTGATGCGACGGTGTTTGGGGGGGCGCGGGTTCGTGCCTTCTCCCCTGGATCACCAACCGAGCAGGCCATGGAGGAAG RKPDDALHRPGGRGPVPFSPGSPTEQSHGGR 1901 ATGARCAGTGGAAGAATGAUGATGGATTGATGAGGGGAATACATGTBANATGTGRCBACAAGGAGAGAGCAAGTTTTGGGTTTGTAGAGTT 2003 TGGCTGCTGCTARTGAGTTGTTGKTAGTGGCTKTATTCTTCAGAACTTCAGATGGTGCCTCACCAAGGCCTAAGAGCCAAGGACGACGACCTTCTGATAATGGT 2101 GTACCTGTCT&CCATCTTTAGTTGGCGGGGTGTTCTTTCCTAGTTGGCACCTTGCATGTARATTCARATTCTCCCCCAAAATAGATTTGTGTGTATAATAA 2301 TTTTGCTTGGTTGAAAAAAAAAAAAAAAA

<u>.</u>

Figure 2

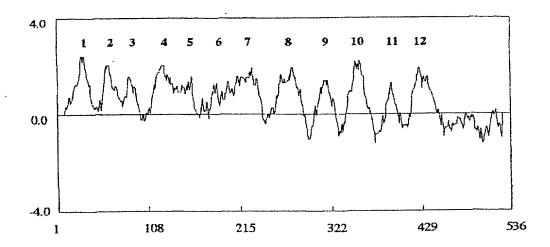
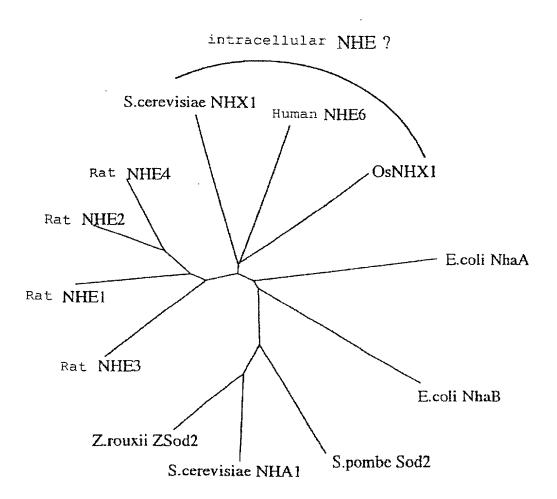


Figure 3

	Α	M3	M4	
	OsNHX1	FSEDLFFIYLLPPILFNAGFQVKKKQF	FRNFMTITLFGAVGTMISFFTISIAAIAIFSRM 138	
	NHX1	FNSSYFFNVLLPPITLNSGYELNQVNF	FNNMLSILIFAIPGTFISAVVIGIILYIWTFLG 179	
	NHE6	FDPEVFFNILLPPILFYAGYSLKRRHF	FRNLGSILAYAFLGTAISCFVIGSIMYGCVTLM 205	
	NHE1	LQSDVFFLFLLPPITLDAGYFLPLRQF	TENLGTILIFAVVGTLWNAFFLGGLLYAVCLVG 219	
	NHE2	MKTDVFFLYLLPPIVLDAGYFMPTRPF	FENLGTIFWYAVVGTLWNSIGIGLSLFGICQIE 80	
	NHE3	LTPTLFFFYLLPPIVLDAGYFMPNRLF	FGNLGTILLYAVIGTIWNAATTGLSLYGVFLSG 166	
	NHE4	MDSSIYFLYLLPPIVLESGYFMPTRPF	FENIGSILWWAGLGALINAFGIGLSLYFICQIK 184	
e Fi		**************************************	*: :* :. *: .	
12				
	В	M5	M6	
	OsNHX1	NIGTLDVGDFLAIGAIFSATDS	VCTLQVLNQDET-PFLYSLVFGEGVVNDATSIV 192	
	NHX1	LESIDISFADAMSVGATLSATDP	VTILSIFNAYKVDPKLYTIIFGESLLNDAISIV 235	
	NHE6	KVTGQLAGDFYFTDCLLFGAIVSATDP	VTVLAIFHELQVDVELYALLFGESVLNDAVAIV 265	
STORE	NHE1	GEQINNIGLLUTLLFGSIISAVDP	VAVLAVFEEIHINELLHILVFGESLLNDAVTVV 276	
	NHEZ	AFGLSDITLLQNLLFGSLISAVDP	VAVLAVFENIHVNEQLYILVFGESLLNDAVTVV 137	
	NHE3	LMGELKIGLLDFLLFGSLIAAVDP	VAVLAVFEEVHVNEVLFIIVFGESLLNDAVTVV ZZ3	
	NHE4	AFGLGDINLLONLLFGSLISAVDP	VAVLAVFEEARVNEQLYMMIFGEALLNDGISVV 241	
<u>.</u>		* . * *	* * . * * . * * . *	

Figure 4



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Figure 5

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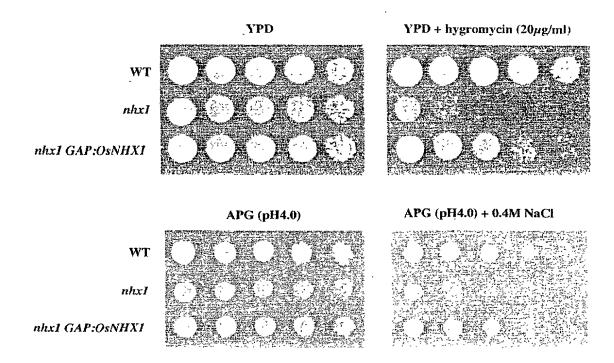


Figure 6

	Ye micr	east cosome	_		Ri	ce				
	nhxI±	±OsNHX1	Root			Shoo	ot	•		
kD	-	+	TM	TP	PM	TM	TP	PM		
97—	****									
97— 66—										
39— 39— 27—	_						<u> Bêrrê</u>	3 A	▼ 0:	sNHX1 40kD)
27—	-									
14—	-			Market Services			: See See See See See See See See See Se	g. Arry they	⋖ V.	-PPase